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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/538,396DATE: 04/19/2000
TIME: 17:20:17

Input Set: I538396.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Mahajan, Pramod B.
2 Shi, Jinrui
3 <120> TITLE OF INVENTION: Maize Rad50 Orthologue and Uses Thereof
4 <130> FILE REFERENCE: 1116
5 <140> CURRENT APPLICATION NUMBER: US/09/538,396
6 <141> CURRENT FILING DATE: 2000-03-29
7 <150> EARLIER APPLICATION NUMBER: 60/132,575
8 <151> EARLIER FILING DATE: 1999-05-05
9 <160> NUMBER OF SEQ ID NOS: 3
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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12 <211> LENGTH: 4492
13 <212> TYPE: DNA
14 <213> ORGANISM: Zea mays
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21 ctccactgcc ctccttttc tctttccaat cgttttgcaa tcactacgag cgtaatgaat 180
22 agaagttgat agggagatag catccgcaat ctaggtttgg ggcaatcgct ctggccagac 240
23 tggatcggag tgcaagtcgt agaggaggc acttggggct cgtggggcaa g atg agc 297
24 Met Ser
25 1
26 acc gtt gac aag atg ctg atc aag ggg att cgg agc ttc gat ccg gac 345
27 Thr Val Asp Lys Met Leu Ile Lys Gly Ile Arg Ser Phe Asp Pro Asp
28 5 10 15
29 aat aag aac gtc atc acc ttc ttc aag ccg ctc acc ctc atc gtt ggc 393
30 Asn Lys Asn Val Ile Thr Phe Phe Lys Pro Leu Thr Leu Ile Val Gly
31 20 25 30
32 ccc aac ggt gct ggc aag acc acg atc atc gag tgc ctg aag ctt tct 441
33 Pro Asn Gly Ala Gly Lys Thr Thr Ile Ile Glu Cys Leu Lys Leu Ser
34 35 40 45 50
35 tgc acc ggc gag ctg ccc ccc aac tcc cgc tct ggc cac acc ttc gtc 489
36 Cys Thr Gly Glu Leu Pro Pro Asn Ser Arg Ser Gly His Thr Phe Val
37 55 60 65
38 cac gac ccc aag gta gct ggc gag acg gaa aca aaa gga caa att aag 537
39 His Asp Pro Lys Val Ala Gly Glu Thr Glu Thr Lys Gly Gln Ile Lys
40 70 75 80
41 ttg cgg ttt aag act gca gca gga aag gat gtg gtg tgc atc cgg tcc 585
42 Leu Arg Phe Lys Thr Ala Ala Gly Lys Asp Val Val Cys Ile Arg Ser
43 85 90 95
44 ttc cag ctt acc caa aag gca tca aag atg gag ttt aag gca att gaa 633
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48	Ser	Val	Leu	Gln	Thr	Ile	Asn	Pro	His	Thr	Gly	Glu	Lys	Val	Cys	Leu	
49		115				120					125				130		
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51	Ser	Tyr	Arg	Cys	Ala	Asp	Met	Asp	Arg	Glu	Ile	Pro	Ala	Leu	Met	Gly	
52				135						140				145			
53	gtt	tcg	aag	gcc	gta	ctg	gag	aat	gtt	ata	ttt	gtt	cac	caa	gat	gaa	777
54	Val	Ser	Lys	Ala	Val	Leu	Glu	Asn	Val	Ile	Phe	Val	His	Gln	Asp	Glu	
55			150					155					160				
56	tcc	aat	tgg	cca	ttg	cag	gac	ccg	tca	aca	ctt	aag	aag	aag	ttc	gat	825
57	Ser	Asn	Trp	Pro	Leu	Gln	Asp	Pro	Ser	Thr	Leu	Lys	Lys	Lys	Phe	Asp	
58		165					170				175						
59	gac	atc	ttc	tct	gcc	aca	cgc	tat	acg	aaa	gct	ctt	gaa	gtc	ata	aag	873
60	Asp	Ile	Phe	Ser	Ala	Thr	Arg	Tyr	Thr	Lys	Ala	Leu	Glu	Val	Ile	Lys	
61		180				185					190						
62	aaa	ctt	cac	aag	gat	caa	atg	caa	gag	atc	aag	act	ttt	agg	tta	aag	921
63	Lys	Leu	His	Lys	Asp	Gln	Met	Gln	Glu	Ile	Lys	Thr	Phe	Arg	Leu	Lys	
64		195				200				205					210		
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66	Leu	Glu	Asn	Leu	Gln	Thr	Val	Lys	Asp	Gln	Ala	His	Lys	Leu	Arg	Glu	
67				215					220				225				
68	aat	att	gct	caa	gat	caa	gaa	aag	tca	gat	gcc	tca	aaa	tct	cag	atg	1017
69	Asn	Ile	Ala	Gln	Asp	Gln	Glu	Lys	Ser	Asp	Ala	Ser	Lys	Ser	Gln	Met	
70			230					235					240				
71	gag	caa	ctg	aag	gaa	aag	atc	tgt	ggc	acc	gag	aga	gaa	atc	ctg	caa	1065
72	Glu	Gln	Leu	Lys	Glu	Lys	Ile	Cys	Gly	Thr	Glu	Arg	Glu	Ile	Leu	Gln	
73		245				250					255						
74	atg	gaa	aca	agt	ttg	gat	gaa	ctg	aga	aga	ctt	cag	gga	caa	att	gac	1113
75	Met	Glu	Thr	Ser	Leu	Asp	Glu	Leu	Arg	Arg	Leu	Gln	Gly	Gln	Ile	Asp	
76		260				265					270						
77	atc	aag	gca	aca	gag	aga	agt	aca	tta	ctt	acg	cag	cag	cat	gaa	aag	1161
78	Ile	Lys	Ala	Thr	Glu	Arg	Ser	Thr	Leu	Leu	Thr	Gln	Gln	His	Glu	Lys	
79		275				280					285				290		
80	ctt	gct	gca	ctt	tct	gag	gaa	aat	gaa	gat	acc	gat	gag	gaa	cta	atg	1209
81	Leu	Ala	Ala	Leu	Ser	Glu	Glu	Asn	Glu	Asp	Thr	Asp	Glu	Glu	Leu	Met	
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83	gaa	tgg	caa	aca	aaa	ttt	gaa	gaa	agg	att	gcg	tta	cta	gaa	aca	aaa	1257
84	Glu	Trp	Gln	Thr	Lys	Phe	Glu	Glu	Arg	Ile	Ala	Leu	Leu	Glu	Thr	Lys	
85			310					315					320				
86	atc	agt	aaa	ctt	gta	aga	gat	atg	gat	gat	gaa	gca	tct	tat	agc	tcc	1305
87	Ile	Ser	Lys	Leu	Val	Arg	Asp	Met	Asp	Asp	Glu	Ala	Ser	Tyr	Ser	Ser	
88			325				330					335					
89	gtt	ctg	tcc	aaa	caa	aat	tct	gaa	tta	aca	cat	gaa	att	gga	aag	ctc	1353
90	Val	Leu	Ser	Lys	Gln	Asn	Ser	Glu	Leu	Thr	His	Glu	Ile	Gly	Lys	Leu	
91		340				345					350						
92	cag	gca	gaa	gct	gat	gct	cac	ctg	act	atg	aag	cat	gaa	cga	gac	tca	1401
93	Gln	Ala	Glu	Ala	Asp	Ala	His	Leu	Thr	Met	Lys	His	Glu	Arg	Asp	Ser	
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97	375 380 385	
98	cat ccc ttt acg aat gat gtt gct atg aac ctt aca aac agg att aaa	1497
99	His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg Ile Lys	
100	390 395 400	
101	gcg aga cta tca agt ctt gag aat gat ttg ctg gat aag aag aaa tcc	1545
102	Ala Arg Leu Ser Ser Leu Glu Asn Asp Leu Leu Asp Lys Lys Lys Ser	
103	405 410 415	
104	aat gaa gat cag tta gat gtt ttg tgg aaa cac tat ctt aaa ata aat	1593
105	Asn Glu Asp Gln Leu Asp Val Leu Trp Lys His Tyr Leu Lys Ile Asn	
106	420 425 430	
107	gct cgc tac tcc gaa gtt gat ggt cag ata caa tct aag att gaa tcc	1641
108	Ala Arg Tyr Ser Glu Val Asp Gly Gln Ile Gln Ser Lys Ile Glu Ser	
109	435 440 445 450	
110	atg tca ggc att tta aga cgg aga aaa gat aaa gag aaa gaa cgc gat	1689
111	Met Ser Gly Ile Leu Arg Arg Arg Lys Asp Lys Glu Lys Glu Arg Asp	
112	455 460 465	
113	gct gca gaa gtg gag ctt tca aaa ttt aat cta tcc cgt atc gat gag	1737
114	Ala Ala Glu Val Glu Leu Ser Lys Phe Asn Leu Ser Arg Ile Asp Glu	
115	470 475 480	
116	agg gag aga cat atg caa att gaa gtc gag agg aag aca ctt gcg ctt	1785
117	Arg Glu Arg His Met Gln Ile Glu Val Glu Arg Lys Thr Leu Ala Leu	
118	485 490 495	
119	gga gaa aga gac tat gat tca att ata agt cag aaa cga aca gaa gta	1833
120	Gly Glu Arg Asp Tyr Asp Ser Ile Ile Ser Gln Lys Arg Thr Glu Val	
121	500 505 510	
122	tat agt ttg gaa cag aaa ata aaa gtg ctt ctg ccg gag aaa gat ata	1881
123	Tyr Ser Leu Glu Gln Lys Ile Lys Val Leu Leu Arg Glu Lys Asp Ile	
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125	ata aat aga aat gct gat gaa aga gta aaa ctg ggt ttg aag aag gat	1929
126	Ile Asn Arg Asn Ala Asp Glu Arg Val Lys Leu Gly Leu Lys Lys Asp	
127	535 540 545	
128	gca ttg gaa agc agc aag gac aag ctc aat gag ata gtt aat gag cat	1977
129	Ala Leu Glu Ser Ser Lys Asp Lys Leu Asn Glu Ile Val Asn Glu His	
130	550 555 560	
131	aag gat aaa atc aaa aag gta ctt agg ggg agg aat cct ttt gag aag	2025
132	Lys Asp Lys Ile Lys Lys Val Leu Arg Gly Arg Asn Pro Phe Glu Lys	
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134	gat atg aag aag gag atc aat caa gcc ttt tgg cct gtg gac aag gaa	2073
135	Asp Met Lys Lys Glu Ile Asn Gln Ala Phe Trp Pro Val Asp Lys Glu	
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137	tac aat gag tta aga tca aaa tcc cag gaa gca gag caa gag ctt aaa	2121
138	Tyr Asn Glu Leu Arg Ser Lys Ser Gln Glu Ala Glu Gln Glu Leu Lys	
139	595 600 605 610	
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141	Phe Thr Gln Ser Lys Val Thr Asp Ala Arg Glu Gln Leu Thr Lys Leu	
142	615 620 625	
143	cga aga gat atg gat gca aaa aga aga ttc ctg gac tcg aaa ctt caa	2217
144	Arg Arg Asp Met Asp Ala Lys Arg Arg Phe Leu Asp Ser Lys Leu Gln	

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198	Leu Ile Val Glu Lys Lys Leu Leu Glu Glu Ser Leu Asp Pro Leu Ser	
199	915 920 925 930	
200	aaa gag aaa gag agc ttg ttg caa gag tat aat gct ttg aag caa aag	3129
201	Lys Glu Lys Glu Ser Leu Leu Gln Glu Tyr Asn Ala Leu Lys Gln Lys	
202	935 940 945	
203	ctg gat gaa gag tat cat cag ctt gca gaa aga aaa agg gag ttc cag	3177
204	Leu Asp Glu Glu Tyr His Gln Leu Ala Glu Arg Lys Arg Glu Phe Gln	
205	950 955 960	
206	caa gaa ctt gat gct ctt gga aga ctt aat atg aag ata aaa ggg tac	3225
207	Gln Glu Leu Asp Ala Leu Gly Arg Leu Asn Met Lys Ile Lys Gly Tyr	
208	965 970 975	
209	ttg gat tcc aag aaa aac gaa aag ctt aag gaa ttg cag gga agg cat	3273
210	Leu Asp Ser Lys Lys Asn Glu Lys Leu Lys Glu Leu Gln Gly Arg His	
211	980 985 990	
212	gtt ctt tgc cat tct cag tta cag agt tgc atg gca aaa cag caa aga	3321
213	Val Leu Cys His Ser Gln Leu Gln Ser Cys Met Ala Lys Gln Gln Arg	
214	995 1000 1005 1010	
215	ata tca gct gag tta aac aag agc aaa gaa cta ctg cag ggc cag ggc	3369
216	Ile Ser Ala Glu Leu Asn Lys Ser Lys Glu Leu Leu Gln Gly Gln Gly	
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218	cag ttg aaa aga aac att gat gac aat ctc aag tac agg aaa aca aag	3417
219	Gln Leu Lys Arg Asn Ile Asp Asp Asn Leu Lys Tyr Arg Lys Thr Lys	
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221	gct gat gtg gaa caa ctt act cgt gat ata gaa tca ctt gaa gaa agg	3465
222	Ala Asp Val Glu Gln Leu Thr Arg Asp Ile Glu Ser Leu Glu Glu Arg	
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225	Leu Leu Ser Ile Gly Ser Leu Ser Ala Ile Glu Ala Asp Leu Lys Arg	
226	1060 1065 1070	
227	cat tct caa gaa aaa gag agg ctt aat tca gaa ttt aac agg tgg caa	3561
228	His Ser Gln Glu Lys Glu Arg Leu Asn Ser Glu Phe Asn Arg Trp Gln	
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230	gga aca ctt tct gtt tat caa agt aat att tca aag cac aaa caa gag	3609
231	Gly Thr Leu Ser Val Tyr Gln Ser Asn Ile Ser Lys His Lys Gln Glu	
232	1095 1100 1105	
233	ctt aaa ctg tca cag tac aag gat atc gag aag cga tat act aat caa	3657
234	Leu Lys Leu Ser Gln Tyr Lys Asp Ile Glu Lys Arg Tyr Thr Asn Gln	
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236	ttt ctc cag ctt aag aca act gaa atg gca aac aag gac ttg gac aga	3705
237	Phe Leu Gln Leu Lys Thr Thr Glu Met Ala Asn Lys Asp Leu Asp Arg	
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239	tat tat act gct tta gac aag gct ctt atg cgg ttc cac agc atg aag	3753
240	Tyr Tyr Thr Ala Leu Asp Lys Ala Leu Met Arg Phe His Ser Met Lys	
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242	atg gag gag ata aat aaa ata atc aag gaa ctg tgg caa cag aca tac	3801
243	Met Glu Glu Ile Asn Lys Ile Ile Lys Glu Leu Trp Gln Gln Thr Tyr	
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VERIFICATION SUMMARY
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Line ? Error/Warning

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